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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/852,053

DATE: 08/07/2001
TIME: 13:32:58

Input Set : A:\Ma280248.app
Output Set: N:\CRF3\08072001\I852053.raw

3 <110> APPLICANT: BERENS, STEPHAN
 4 KALINOWSKI, JORN
 5 PUHLER, ALFRED
 7 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM STRAIN WITH
 8 ENHANCED SECRETION ACTIVITY
 10 <130> FILE REFERENCE: MAS/21123/280248
 12 <140> CURRENT APPLICATION NUMBER: 09/852,053
 13 <141> CURRENT FILING DATE: 2001-05-10
 15 <150> PRIOR APPLICATION NUMBER: EPO 00110021.3
 16 <151> PRIOR FILING DATE: 2000-05-12
 18 <160> NUMBER OF SEQ ID NOS: 24
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1960
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Corynebacterium glutamicum
 27 <220> FEATURE:
 28 <221> NAME/KEY: misc_feature
 29 <222> LOCATION: (34)..(1944)
 30 <223> OTHER INFORMATION: secD
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 35 gtttatgcgt tgggtctgtt gacaggcgat cggtctgcca caccaaaatt gggatttgat 180
 36 ctgcaaggcg gaaccggagt gaccctcgta ccgcaggggc aggatccaac tcaggaccag 240
 37 ctgaatcagg cacgcaccat tctggaaaac cggtgtaaacg gcatggcggt ttcaggtgca 300
 38 agcgtggtcg ctgacggtaa cacgctgggt atcactgttc ccggggaaaa taccgcacag 360
 39 ggcataatccc taggacagac ctcccagctg ctgttccgtc ccgttgggtca ggcaggaatg 420
 40 cccgatatac ccacgttgc gccagagctg gaagagatgg ccaacagggtg gttgaatac 480
 41 ggcgtcatca ccgaagagca ggcaaatgcc tccttggagg aaatgaacac cgctgttgca 540
 42 tcgaccactg cggtgtaaagg cgaagaagca actgagccag aaccgcgtcac cggtgtggcg 600
 43 acccctatgg atgagccagc caactccatt gaggcaacac agcgcacgcca gaaatcagc 660
 44 gacatgctgc gcaccgaccg ccagtccacc gatcccactg tccagatcgc tgcaagttct 720
 45 ttgtatcgatg gcaccactga tgagatggat cctttggccg gcaccgtatga tccacgcctg 780
 46 ccattgggtgg catgtatcc agctgttagt ggcgtgtatg tacttgatcc tgacaccttg 840
 47 ctcacggcg aaaccgatga ggaaaatggt ggcgcctaa ccggtaatga gatgataacc 900
 48 aaccgtcccc tcaccgggtt attcaacgccc cagtcggcc agatggaaat cagcttgcc 960
 49 ttcaaatccg gcgatgggaa agaaggctct gcaacttggat cctctctgac cagccagttac 1020
 50 ctgcagcagc agatcgccat caccctggac tctcaggatg tttctgcacc cgtgattcag 1080
 51 tcagcaaccc ctgtgggttc tgcaacatcc atcaccgggtg acttcactca aactgaagcc 1140
 52 caagatctgg cgaacaacct ggcgtacggt gcattgcccc tggatctgcg aggtgaaaac 1200
 53 ggcgagcgcg gcgaaactac caccaccgtt cgcgcacac taggcgcagc atccttgaag 1260
 54 gccggactga tcgcaggcat cgccggatc ggcgtggcg ccatcttgcgt gttccctac 1320
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 56 ggccttctgg tactgtgggg acgctggatc ggatattccc tagaccttgc tggtatcgcc 1440
 57 gtttgcgtca tcggatcg taccaccggc gactcctcg tggtgttcta tgagcgcac 1500
 58 aaggatgaga tccgtgaagg aagatcctt agatctgcag tacctcgtgc atggaaagc 1560

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59 gccaaggcga ccatcgtaac aggcaacatg gtcactttgc tcggcgctat cgtgatttac 1620
 60 ttgctcgccg tcggcgaagt caagggctt gccttcaccc tgggtctgac caccgtattc 1680
 61 gatctcggtt tcacacctt gatcacggca ccactggta tcctggcatc acgaaccca 1740
 62 ttctttgcca agtcatcggt caacggcatg ggacgagtga tgaagctcgt tgaagaacgc 1800
 63 cgcgccaacg gtgaatttggaa tgagcctgag tacctgaaaa agatccatgc caagaatgcg 1860
 64 gcagctgata aggcttccac tgacaattct tccactgaca attctgaagc acctggcacc 1920
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 81 gacttcatcg ccaaaaccaa actgtggta tggatcaccc gcattttgtt gtttatctcg 180
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 84 accggcattt ctccggaaat cgtgcagatc gtcggttccg ggcacgccc accctggag 360
 85 atctactccg agcgcactcgat cgatgaggat gtagaaaaag cccgcctgac gatctacgag 420
 86 gaataccaaac ccctaaaactc tgaggggccag ccaagcccaat atgcacatcg taattccacg 480
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 89 atggcagcat tggttgttga cggcatcgatc atcgccggca totacggcgat catcgccctc 660
 90 gaagtatccc cagcaaccgt catcggtctg ctcaccgtgc tgaccccttc catctacgac 720
 91 accgtcggtt tctttgacaa ggtcagagaaa aacaccgaag gcttcgaagg cagccgcaga 780
 92 cgaacctacg ccgaacaacgc caacctggcg gtcaaccaga cttcatcgat ttcgatctcc 840
 93 acgacaatca tctctgcaact tccgatcatc gctttgatgg ttgtcgccgt ctggatgatg 900
 94 ggtgtggca ccctcaaaga cctcgactg atccagctga tcggcgatcat cgaaggcacc 960
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 97 gccacccac acaccaacgc cgacgcctcc ggcacggca cggaaaggcga cactgacgg 1140
 98 gtgacccccc aagcacctgc aaaacgtaca gtaagcaaac ccattgtggta tgatcaccga 1200
 99 tcaagcggaa cctggcgacc aggcagaacg taaaccaatt ggagaacgaa gaaaaatccc 1260
 100 gcagactcgc gttctgcggg attttttttg tgcgtctatg actcacgatg ttcccaaacg 1320
 101 acgacttcac gtggcgact tcagtcggat ttgcgtttt tatccagtgatc agtccggctca 1380
 102 tgagaagttt agcacgcgaa gtcgttaggtt gaggtctcgat aatctgcggt gtcgttaggtt 1440
 103 gagatgtcgc cgcccttaagt tcgatccatc accttcgata cctcacgctc aatttcttat 1500
 104 gttcgagacc gcttaggaaaa gcaccaaaaa ccgactgaaa ttgagtttgg gaaatttgagc 1560
 105 gc 1562
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 109 <211> LENGTH: 637
 110 <212> TYPE: PRT
 111 <213> ORGANISM: Corynebacterium glutamicum
 113 <220> FEATURE:
 114 <221> NAME/KEY: PROPEP

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115 <222> LOCATION: (1)..(637)
 116 <223> OTHER INFORMATION: secD
 118 <400> SEQUENCE: 3
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 122 Lys Arg Ala Ile Ala Leu Phe Val Leu Ile Val Val Gly Val Tyr Ala
 123 20 25 30
 125 Leu Val Leu Leu Thr Gly Asp Arg Ser Ala Thr Pro Lys Leu Gly Ile
 126 35 40 45
 128 Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro Gln Gly Gln Asp
 129 50 55 60
 131 Pro Thr Gln Asp Gln Leu Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg
 132 65 70 75 80
 134 Val Asn Gly Met Gly Val Ser Gly Ala Ser Val Val Ala Asp Gly Asn
 135 85 90 95
 137 Thr Leu Val Ile Thr Val Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser
 138 100 105 110
 140 Leu Gly Gln Thr Ser Gln Leu Leu Phe Arg Pro Val Gly Gln Ala Gly
 141 115 120 125
 143 Met Pro Asp Met Thr Thr Leu Met Pro Glu Leu Glu Glu Met Ala Asn
 144 130 135 140
 146 Arg Trp Val Glu Tyr Gly Val Ile Thr Glu Glu Gln Ala Asn Ala Ser
 147 145 150 155 160
 149 Leu Glu Glu Met Asn Thr Ala Val Ala Ser Thr Thr Ala Val Glu Gly
 150 165 170 175
 152 Glu Glu Ala Thr Glu Pro Glu Pro Val Thr Val Ser Ala Thr Pro Met
 153 180 185 190
 155 Asp Glu Pro Ala Asn Ser Ile Glu Ala Thr Gln Arg Arg Gln Glu Ile
 156 195 200 205
 158 Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp Pro Thr Val Gln
 159 210 215 220
 161 Ile Ala Ala Ser Ser Leu Met Gln Cys Thr Thr Asp Glu Met Asp Pro
 162 225 230 235 240
 164 Leu Ala Gly Thr Asp Asp Pro Arg Leu Pro Leu Val Ala Cys Asp Pro
 165 245 250 255
 167 Ala Val Gly Gly Val Tyr Val Leu Asp Pro Ala Pro Leu Leu Asn Gly
 168 260 265 270
 170 Glu Thr Asp Glu Glu Asn Gly Ala Arg Leu Thr Gly Asn Glu Ile Asp
 171 275 280 285
 173 Thr Asn Arg Pro Ile Thr Gly Gly Phe Asn Ala Gln Ser Gly Gln Met
 174 290 295 300
 176 Glu Ile Ser Phe Ala Phe Lys Ser Gly Asp Gly Glu Glu Gly Ser Ala
 177 305 310 315 320
 179 Thr Trp Ser Ser Leu Thr Ser Gln Tyr Leu Gln Gln Ile Ala Ile
 180 325 330 335
 182 Thr Leu Asp Ser Gln Val Ile Ser Ala Pro Val Ile Gln Ser Ala Thr
 183 340 345 350
 185 Pro Val Gly Ser Ala Thr Ser Ile Thr Gly Asp Phe Thr Gln Thr Glu
 186 355 360 365

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188 Ala Gln Asp Leu Ala Asn Asn Leu Arg Tyr Gly Ala Leu Pro Leu Ser
 189 370 375 380
 191 Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr Thr Thr Val Pro
 192 385 390 395 400
 194 Pro Ser Leu Gly Ala Ala Ser Leu Lys Ala Gly Leu Ile Ala Gly Ile
 195 405 410 415
 197 Val Gly Ile Ala Leu Val Ala Ile Phe Val Phe Ala Tyr Tyr Arg Val
 198 420 425 430
 200 Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala Gly Val Leu Val
 201 435 440 445
 203 Tyr Gly Leu Leu Val Leu Leu Gly Arg Trp Ile Gly Tyr Ser Leu Asp
 204 450 455 460
 206 Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly Thr Thr Ala Asp
 207 465 470 475 480
 209 Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu Ile Arg Glu Gly
 210 485 490 495
 212 Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu Ser Ala Lys Arg
 213 500 505 510
 215 Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly Ala Ile Val Ile
 216 515 520 525
 218 Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala Phe Thr Leu Gly
 219 530 535 540
 221 Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu Ile Thr Ala Pro
 222 545 550 555 560
 224 Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala Lys Ser Ser Val
 225 565 570 575
 227 Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu Arg Arg Ala Asn
 228 580 585 590
 230 Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile His Ala Lys Asn
 231 595 600 605
 233 Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser Thr Asp Asn Ser
 234 610 615 620
 236 Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu Lys
 237 625 630 635
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 241 <211> LENGTH: 403
 242 <212> TYPE: PRT
 243 <213> ORGANISM: Corynebacterium glutamicum
 245 <220> FEATURE:
 246 <221> NAME/KEY: PROPEP
 247 <222> LOCATION: (1)..(403)
 248 <223> OTHER INFORMATION: secF
 250 <400> SEQUENCE: 4
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 252 1 5 10 15
 254 Ala Lys Lys Arg Ser Trp Phe Asn Ser Leu Tyr Thr Gly Asp Gly Gly
 255 20 25 30
 257 Ile Asp Phe Ile Ala Lys Thr Lys Leu Trp Tyr Trp Ile Thr Gly Ile
 258 35 40 45

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260 Leu Leu Val Ile Ser Ile Leu Phe Ile Ala Ile Arg Gly Phe Ser Leu
 261 50 55 60
 263 Ser Ile Asp Phe Gln Gly Gly Thr Lys Met Ser Met Pro Ala Ser Asp
 264 65 70 75 80
 266 Tyr Ser Thr Glu Gln Val Glu Glu Thr Phe Thr Glu Ala Thr Gly Ile
 267 85 90 95
 269 Thr Pro Glu Ile Val Gln Ile Val Gly Ser Gly Asp Ala Arg Thr Leu
 270 100 105 110
 272 Glu Ile Tyr Ser Glu Arg Leu Ser Asp Glu Asp Val Glu Lys Ala Arg
 273 115 120 125
 275 Leu Ala Ile Tyr Glu Glu Tyr Gln Pro Leu Asn Ser Glu Gly Gln Pro
 276 130 135 140
 278 Ser Pro Asp Ala Ile Gly Asn Ser Thr Val Ser Glu Ser Trp Gly Ser
 279 145 150 155 160
 281 Thr Ile Thr Gln Arg Met Val Leu Ala Leu Ile Ala Phe Leu Val Ile
 282 165 170 175
 284 Ala Ala Ile Tyr Ile Ala Phe Arg Leu Glu Arg Glu Met Ala Ile Ala
 285 180 185 190
 287 Ala Met Ala Ala Leu Val Val Asp Gly Ile Val Ile Ala Gly Ile Tyr
 288 195 200 205
 290 Ala Val Ile Gly Leu Glu Val Ser Pro Ala Thr Val Ile Gly Leu Leu
 291 210 215 220
 293 Thr Val Leu Thr Phe Ser Ile Tyr Asp Thr Val Val Val Phe Asp Lys
 294 225 230 235 240
 296 Val Arg Glu Asn Thr Glu Gly Phe Glu Gly Ser Arg Arg Arg Thr Tyr
 297 245 250 255
 299 Ala Glu Gln Ala Asn Leu Ala Val Asn Gln Thr Phe Met Arg Ser Ile
 300 260 265 270
 302 Ser Thr Thr Ile Ile Ser Ala Leu Pro Ile Ile Ala Leu Met Val Val
 303 275 280 285
 305 Ala Val Trp Met Met Gly Val Gly Thr Leu Lys Asp Leu Ala Leu Ile
 306 290 295 300
 308 Gln Leu Ile Gly Val Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala
 309 305 310 315 320
 311 Thr Pro Leu Leu Val Ser Leu Lys Asn Arg Leu Ser Lys Thr Lys Ala
 312 325 330 335
 314 His Thr Ala Ser Val Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile
 315 340 345 350
 317 Asp Ala Thr Pro His Thr Asn Ala Asp Ala Ser Ala His Gly Thr Glu
 318 355 360 365
 320 Ser Asp Thr Asp Gly Val Thr Pro Glu Ala Pro Ala Lys Arg Thr Val
 321 370 375 380
 323 Ser Lys Pro Ile Val Asp Asp His Arg Ser Ser Gly Thr Trp Arg Pro
 324 385 390 395 400
 326 Gly Arg Ser
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 330 <211> LENGTH: 20
 331 <212> TYPE: DNA
 332 <213> ORGANISM: Artificial Sequence

VERIFICATION SUMMARY

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